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SEQUENCE LISTING

5 (1) GENERAL INFORMATION:

(i) APPLICANT:

10 (A) NAME: ACTINOVA LIMITED
(B) STREET: 5 Signet Court, Swanns Road
(C) CITY: Cambridge
(E) COUNTRY: United Kingdom
(F) POSTAL CODE (ZIP): CB5 8LA

15 (ii) TITLE OF INVENTION: IMMUNOGLOBULIN BINDING PROTEIN

(iii) NUMBER OF SEQUENCES: 22

(iv) COMPUTER READABLE FORM:

20 (A) MEDIUM TYPE: Floppy disk
(B) COMPUTER: IBM PC compatible
(C) OPERATING SYSTEM: PC-DOS/MS-DOS
(D) SOFTWARE: PatentIn Release #1.0, Version #1.30 (EPO)

(v) CURRENT APPLICATION DATA:

25 APPLICATION NUMBER: GB N/A

(2) INFORMATION FOR SEQ ID NO: 1:

(i) SEQUENCE CHARACTERISTICS:

30 (A) LENGTH: 249 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

35 (ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

40 (A) NAME/KEY: CDS
(B) LOCATION: 1..246

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1:

45	ATG AAC ATT AAA TTT GCT GGA AAA GAA ACA CCA GAA ACA CCA GAA GAA	48
	Met Asn Ile Lys Phe Ala Gly Lys Glu Thr Pro Glu Thr Pro Glu Glu	
	1 5 10 15	
50	CCA AAA GAA GAA GTT ACA ATC AAA GTT AAC TTA ATC TTT GCA GAT GGA	96
	Pro Lys Glu Glu Val Thr Ile Lys Val Asn Leu Ile Phe Ala Asp Gly	
	20 25 30	

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5 AAG ATA CAA ACA GCA GAA TTC AAA GGA ACA TTT GAA GAA GCA ACA GCA 144
 Lys Ile Gln Thr Ala Glu Phe Lys Gly Thr Phe Glu Glu Ala Thr Ala
 35 40 45

 10 GAA GCT TAC AGA TAT GCA GAC TTA TTA GCA AAA GTA AAT GGC GAA TAT 192
 Glu Ala Tyr Arg Tyr Ala Asp Leu Leu Ala Lys Val Asn Gly Glu Tyr
 50 55 60

 15 ACA GCA GAC TTA GAA GAT GGT GGA AAC CAT ATG AAC ATT AAA TTT GCT 240
 Thr Ala Asp Leu Glu Asp Gly Gly Asn His Met Asn Ile Lys Phe Ala
 65 70 75 80

 20 GGA AAA TAA 249
 Gly Lys

20 (2) INFORMATION FOR SEQ ID NO: 2:

 (1) SEQUENCE CHARACTERISTICS:

 (A) LENGTH: 82 amino acids

 (B) TYPE: amino acid

25 (D) TOPOLOGY: linear

 (11) MOLECULE TYPE: protein

 (x1) SEQUENCE DESCRIPTION: SEQ ID NO: 2:

30 Met Asn Ile Lys Phe Ala Gly Lys Glu Thr Pro Glu Thr Pro Glu Glu
 1 5 10 15

 Pro Lys Glu Glu Val Thr Ile Lys Val Asn Leu Ile Phe Ala Asp Gly
 20 25 30
 35 Lys Ile Gln Thr Ala Glu Phe Lys Gly Thr Phe Glu Glu Ala Thr Ala
 35 40 45

 Glu Ala Tyr Arg Tyr Ala Asp Leu Leu Ala Lys Val Asn Gly Glu Tyr
 50 55 60

 Thr Ala Asp Leu Glu Asp Gly Gly Asn His Met Asn Ile Lys Phe Ala
 65 70 75 80
 45 Gly Lys

(2) INFORMATION FOR SEQ ID NO: 3:

50 (i) SEQUENCE CHARACTERISTICS:

 (A) LENGTH: 228 base pairs

 (B) TYPE: nucleic acid

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(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

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(1) MOLECULE TYPE: DNA (genomic)

(1x) FEATURE:

10

(A) NAME/KEY: CDS

(B) LOCATION:1..228

(x1) SEQUENCE DESCRIPTION: SEQ ID NO: 3:

15

AAA GAA GAA ACA CCA GAA ACA CCA GAA ACT GAT TCA GAA GAA GAA GTA	48
Lys Glu Glu Thr Pro Glu Thr Pro Glu Thr Asp Ser Glu Glu Glu Val	
235 240 245	

20

ACA ATC AAA GCT AAC CTA ATC TTT GCA AAT GGA AGC ACA CAA ACT GCA	96
Thr Ile Lys Ala Asn Leu Ile Phe Ala Asn Gly Ser Thr Gln Thr Ala	
250 255 260 265	

25

GAA TTC AAA GGA ACA TTT GAA AAA GCA ACA TCA GAA GCT TAT GCG TAT	144
Glu Phe Lys Gly Thr Phe Glu Lys Ala Thr Ser Glu Ala Tyr Ala Tyr	
270 275 280	

30

GCA GAT ACT TTG AAG AAA GAC AAT GGA GAA TAT ACT GTA GAT GTT GCA	192
Ala Asp Thr Leu Lys Lys Asp Asn Gly Glu Tyr Thr Val Asp Val Ala	
285 290 295	

35

GAT AAA GGT TAT ACT TTA AAT ATT AAA TTT GCT GGA	228
Asp Lys Gly Tyr Thr Leu Asn Ile Lys Phe Ala Gly	
300 305	

(2) INFORMATION FOR SEQ ID NO: 4:

(i) SEQUENCE CHARACTERISTICS:

40

(A) LENGTH: 76 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

45

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4:

Lys Glu Glu Thr Pro Glu Thr Pro Glu Thr Asp Ser Glu Glu Glu Val
1 5 10 15

50

Thr Ile Lys Ala Asn Leu Ile Phe Ala Asn Gly Ser Thr Gln Thr Ala
20 25 30

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5 Glu Phe Lys Gly Thr Phe Glu Lys Ala Thr Ser Glu Ala Tyr Ala Tyr
 35 40 45

Ala Asp Thr Leu Lys Lys Asp Asn Gly Glu Tyr Thr Val Asp Val Ala
 50 55 60

10 Asp Lys Gly Tyr Thr Leu Asn Ile Lys Phe Ala Gly
 65 70 75

(2) INFORMATION FOR SEQ ID NO: 5:

15 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 216 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

20 (ii) MOLECULE TYPE: DNA (genomic)

25 (i) FEATURE:
 (A) NAME/KEY: CDS
 (B) LOCATION: 1..216

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5:

30 AAA GAA AAA ACA CCA GAA GAA CCA AAA GAA GAA GTT ACT ATT AAA GCA 48
 Lys Glu Lys Thr Pro Glu Glu Pro Lys Glu Glu Val Thr Ile Lys Ala
 80 85 90

35 AAC TTA ATC TAT GCA GAT GGA AAA ACA CAA ACA GCA GAA TTC AAA GGA 96
 Asn Leu Ile Tyr Ala Asp Gly Lys Thr Gln Thr Ala Glu Phe Lys Gly
 95 100 105

40 ACA TTT GAA GAA GCA ACA GCA GAA GCA TAC AGA TAT GCA GAT GCA TTA 144
 Thr Phe Glu Glu Ala Thr Ala Glu Ala Tyr Arg Tyr Ala Asp Ala Leu
 110 115 120

45 AAG AAG GAC AAT GGA GAA TAT ACA GTA GAC GTT GCA GAT AAA GGT TAT 192
 Lys Lys Asp Asn Gly Glu Tyr Thr Val Asp Val Ala Asp Lys Gly Tyr
 125 130 135 140

50 ACT TTA AAT ATT AAA TTT GCT GGA 216
 Thr Leu Asn Ile Lys Phe Ala Gly
 145

(2) INFORMATION FOR SEQ ID NO: 6:

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(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 72 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 6:

Lys Glu Lys Thr Pro Glu Glu Pro Lys Glu Glu Val Thr Ile Lys Ala
 1 5 10 15

Asn Leu Ile Tyr Ala Asp Gly Lys Thr Gln Thr Ala Glu Phe Lys Gly
 20 25 30

Thr Phe Glu Glu Ala Thr Ala Glu Ala Tyr Arg Tyr Ala Asp Ala Leu
 35 40 45

Lys Lys Asp Asn Gly Glu Tyr Thr Val Asp Val Ala Asp Lys Gly Tyr
 50 55 60

Thr Leu Asn Ile Lys Phe Ala Gly
 65 70

(2) INFORMATION FOR SEQ ID NO: 7:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 216 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

(A) NAME/KEY: CDS

(B) LOCATION:1..216

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 7:

AAA GAA AAA ACA CCA GAA GAA CCA AAA GAA GAA GTT ACT ATT AAA GCA 48
 Lys Glu Lys Thr Pro Glu Glu Pro Lys Glu Glu Val Thr Ile Lys Ala
 75 80 85

AAC TTA ATC TAT GCA GAT GGA AAA ACA CAA ACA GCA GAA TTC AAA GGA 96
 Asn Leu Ile Tyr Ala Asp Gly Lys Thr Gln Thr Ala Glu Phe Lys Gly
 90 95 100

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5 ACA TTT GAA GAA GCA ACA GCA GAA GCA TAC AGA TAT GCT GAC TTA TTA 144
 Thr Phe Glu Glu Ala Thr Ala Glu Ala Tyr Arg Tyr Ala Asp Leu Leu
 105 110 115 120

 10 GCA AAA GAA AAT GGT AAA TAT ACA GTA GAC GTT GCA GAT AAA GGT TAT 192
 Ala Lys Glu Asn Gly Lys Tyr Thr Val Asp Val Ala Asp Lys Gly Tyr
 125 130 135

 ACT TTA AAT ATT AAA TTT GCT GGA 216
 Thr Leu Asn Ile Lys Phe Ala Gly
 140

(2) INFORMATION FOR SEQ ID NO: 8:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 72 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 8:

25 Lys Glu Lys Thr Pro Glu Glu Pro Lys Glu Glu Val Thr Ile Lys Ala
 1 5 10 15

 30 Asn Leu Ile Tyr Ala Asp Gly Lys Thr Gln Thr Ala Glu Phe Lys Gly
 20 25 30

 Thr Phe Glu Glu Ala Thr Ala Glu Ala Tyr Arg Tyr Ala Asp Leu Leu
 35 40 45

 35 Ala Lys Glu Asn Gly Lys Tyr Thr Val Asp Val Ala Asp Lys Gly Tyr
 50 55 60

 Thr Leu Asn Ile Lys Phe Ala Gly
 65 70

(2) INFORMATION FOR SEQ ID NO: 9:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 216 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

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(A) NAME/KEY: CDS
(B) LOCATION:1..216

5

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 9:

10 AAA GAA AAA ACA CCA GAA GAA CCA AAA GAA GAA GTT ACT ATT AAA GCA 48
 Lys Glu Lys Thr Pro Glu Glu Pro Lys Glu Glu Val Thr Ile Lys Ala
 75 80 85

15 AAC TTA ATC TAT GCA GAT GGA AAA ACT CAA ACA GCA GAG TTC AAA GGA 96
 Asn Leu Ile Tyr Ala Asp Gly Lys Thr Gln Thr Ala Glu Phe Lys Gly
 90 95 100

20 ACA TTT GCA GAA GCA ACA GCA GAA GCA TAC AGA TAC GCT GAC TTA TTA 144
 Thr Phe Ala Glu Ala Thr Ala Glu Ala Tyr Arg Tyr Ala Asp Leu Leu
 105 110 115 120

25 GCA AAA GAA AAT GGT AAA TAT ACA GCA GAC TTA GAA GAT GGT GGA TAC 192
 Ala Lys Glu Asn Gly Lys Tyr Thr Ala Asp Leu Glu Asp Gly Gly Tyr
 125 130 135

25 ACT ATT AAT ATT AGA TTT GCA GGT 216
 Thr Ile Asn Ile Arg Phe Ala Gly
 140

30 (2) INFORMATION FOR SEQ ID NO: 10:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 72 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

35

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 10:

40 Lys Glu Lys Thr Pro Glu Glu Pro Lys Glu Glu Val Thr Ile Lys Ala
 1 5 10 15

45 Asn Leu Ile Tyr Ala Asp Gly Lys Thr Gln Thr Ala Glu Phe Lys Gly
 20 25 30

45 Thr Phe Ala Glu Ala Thr Ala Glu Ala Tyr Arg Tyr Ala Asp Leu Leu
 35 40 45

50 Ala Lys Glu Asn Gly Lys Tyr Thr Ala Asp Leu Glu Asp Gly Gly Tyr
 50 55 60

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Thr Ile Asn Ile Arg Phe Ala Gly
65 70

5

(2) INFORMATION FOR SEQ ID NO: 11:

(i) SEQUENCE CHARACTERISTICS:

10

- (A) LENGTH: 213 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

15

(ii) MOLECULE TYPE: DNA (genomic)

20

(ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION:1..213

(x) SEQUENCE DESCRIPTION: SEQ ID NO: 11:

25 AAA GAA ACA CCA GAA CCA GAA GAA GTT ACA ATC AAA GCT AAC TTA 48
Lys Glu Thr Pro Glu Pro Glu Glu Glu Val Thr Ile Lys Ala Asn Leu
75 80 85

30 ATC TTT GCA GAT GGA AGC ACA CAA AAT GCA GAA TTC AAA GGA ACA TTC 96
Ile Phe Ala Asp Gly Ser Thr Gln Asn Ala Glu Phe Lys Gly Thr Phe
90 95 100

35 GCA AAA GCA GTA TCA GAT GCT TAC GCT TAC GCA GAT GCT TTA AAG AAA 144
Ala Lys Ala Val Ser Asp Ala Tyr Ala Tyr Ala Asp Ala Leu Lys Lys
105 110 115 120

GAC AAC GGA GAA TAT ACT GTA GAC GTT GCA GAT AAA GGC TTA ACT TTA 192
Asp Asn Gly Glu Tyr Thr Val Asp Val Ala Asp Lys Gly Leu Thr Leu
125 130 135

40 AAT ATT AAA TTC GCT GGT AAA 213
Asn Ile Lys Phe Ala Gly Lys
140

45 (2) INFORMATION FOR SEQ ID NO: 12:

(i) SEQUENCE CHARACTERISTICS:

50

- (A) LENGTH: 71 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

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(x1) SEQUENCE DESCRIPTION: SEQ ID NO: 12:

5 Lys Glu Thr Pro Glu Pro Glu Glu Glu Val Thr Ile Lys Ala Asn Leu
 1 5 10 15
 Ile Phe Ala Asp Gly Ser Thr Gln Asn Ala Glu Phe Lys Gly Thr Phe
 20 25 30
 10 Ala Lys Ala Val Ser Asp Ala Tyr Ala Tyr Ala Asp Ala Leu Lys Lys
 35 40 45
 15 Asp Asn Gly Glu Tyr Thr Val Asp Val Ala Asp Lys Gly Leu Thr Leu
 50 55 60
 Asn Ile Lys Phe Ala Gly Lys
 65 70

20

(2) INFORMATION FOR SEQ ID NO: 13:

(1) SEQUENCE CHARACTERISTICS:

25 (A) LENGTH: 213 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

30

(11) MOLECULE TYPE: DNA (genomic)

(1x) FEATURE:

35 (A) NAME/KEY: CDS
 (B) LOCATION: 1..213

35

(x1) SEQUENCE DESCRIPTION: SEQ ID NO: 13:

40 AAA GAA AAA CCA GAA GAA CCA AAA GAA GAA GTT ACA ATC AAA GTT AAC 48
 Lys Glu Lys Pro Glu Glu Pro Lys Glu Glu Val Thr Ile Lys Val Asn
 75 80 85
 TTA ATC TTT GCA GAT GGA AAG ACA CAA ACA GCA GAA TTC AAA GGA ACA 96
 Leu Ile Phe Ala Asp Gly Lys Thr Gln Thr Ala Glu Phe Lys Gly Thr
 90 95 100
 TTT GAA GAA GCA ACA GCA AAA GCT TAT GCT TAT GCA GAC TTA TTA GCA 144
 Phe Glu Glu Ala Thr Ala Lys Ala Tyr Ala Tyr Ala Asp Leu Leu Ala
 105 110 115
 50

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AAA GAA AAT GGC GAA TAT ACA GCA GAC TTA GAA GAT GGT GGA AAC ACA 192
 Lys Glu Asn Gly Glu Tyr Thr Ala Asp Leu Glu Asp Gly Gly Asn Thr
 5 120 125 130 135

ATC AAC ATT AAA TTT GCT GGA 213
 Ile Asn Ile Lys Phe Ala Gly
 140

10

(2) INFORMATION FOR SEQ ID NO: 14:

(i) SEQUENCE CHARACTERISTICS:
 15 (A) LENGTH: 71 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein
 20 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 14:

Lys Glu Lys Pro Glu Glu Pro Lys Glu Glu Val Thr Ile Lys Val Asn
 1 5 10 15

25 Leu Ile Phe Ala Asp Gly Lys Thr Gln Thr Ala Glu Phe Lys Gly Thr
 20 25 30

Phe Glu Glu Ala Thr Ala Lys Ala Tyr Ala Tyr Ala Asp Leu Leu Ala
 35 40 45

30 Lys Glu Asn Gly Glu Tyr Thr Ala Asp Leu Glu Asp Gly Gly Asn Thr
 50 55 60

35 Ile Asn Ile Lys Phe Ala Gly
 65 70

(2) INFORMATION FOR SEQ ID NO: 15:

(i) SEQUENCE CHARACTERISTICS:
 40 (A) LENGTH: 222 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

45 (ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:
 (A) NAME/KEY: CDS
 50 (B) LOCATION:1..222

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 15:

5 AAA GAA ACA CCA GAA ACA CCA GAA GAA CCA AAA GAA GAA GTT ACA ATC 48
 Lys Glu Thr Pro Glu Thr Pro Glu Glu Pro Lys Glu Glu Val Thr Ile
 75 80 85

10 AAA GTT AAC TTA ATC TTT GCA GAT GGA AAG ATA CAA ACA GCA GAA TTC 96
 Lys Val Asn Leu Ile Phe Ala Asp Gly Lys Ile Gln Thr Ala Glu Phe
 90 95 100

15 AAA GGA ACA TTT GAA GAA GCA ACA GCA AAA GCT TAT GCT TAT GCA AAC 144
 Lys Gly Thr Phe Glu Glu Ala Thr Ala Lys Ala Tyr Ala Tyr Ala Asn
 105 110 115

20 TTA TTA GCA AAA GAA AAT GGC GAA TAT ACA GCA GAC TTA GAA GAT GGT 192
 Leu Leu Ala Lys Glu Asn Gly Glu Tyr Thr Ala Asp Leu Glu Asp Gly
 120 125 130 135

25 GGA AAC ACA ATC AAC ATT AAA TTT GCT GGA 222
 Gly Asn Thr Ile Asn Ile Lys Phe Ala Gly
 140 145

(2) INFORMATION FOR SEQ ID NO: 16:

(i) SEQUENCE CHARACTERISTICS:

30 (A) LENGTH: 74 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 16:

35 Lys Glu Thr Pro Glu Thr Pro Glu Glu Pro Lys Glu Glu Val Thr Ile
 1 5 10 15

40 Lys Val Asn Leu Ile Phe Ala Asp Gly Lys Ile Gln Thr Ala Glu Phe
 20 25 30

45 Lys Gly Thr Phe Glu Glu Ala Thr Ala Lys Ala Tyr Ala Tyr Ala Asn
 35 40 45

50 Leu Leu Ala Lys Glu Asn Gly Glu Tyr Thr Ala Asp Leu Glu Asp Gly
 50 55 60

55 Gly Asn Thr Ile Asn Ile Lys Phe Ala Gly
 65 70

(2) INFORMATION FOR SEQ ID NO: 17:

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(1) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 225 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(11) MOLECULE TYPE: DNA (genomic)

(1x) FEATURE:

- (A) NAME/KEY: CDS
 (B) LOCATION: 1..225

(x1) SEQUENCE DESCRIPTION: SEQ ID NO: 17:

AAA GAA ACA CCA GAA ACA CCA GAA GAA CCA AAA GAA GAA GTT ACA ATC 48
 Lys Glu Thr Pro Glu Thr Pro Glu Glu Pro Lys Glu Glu Val Thr Ile
 75 80 85 90

AAA GTT AAC TTA ATC TTT GCA GAT GGA AAA ACA CAA ACA GCA GAA TTC 96
 Lys Val Asn Leu Ile Phe Ala Asp Gly Lys Thr Gln Thr Ala Glu Phe
 95 100 105

AAA GGA ACA TTT GAA GAA GCA ACA GCA GAA GCT TAC AGA TAT GCA GAC 144
 Lys Gly Thr Phe Glu Glu Ala Thr Ala Glu Ala Tyr Arg Tyr Ala Asp
 110 115 120

TTA TTA GCA AAA GTA AAT GGT GAA TAC ACA GCA GAC TTA GAA GAT GGC 192
 Leu Leu Ala Lys Val Asn Gly Glu Tyr Thr Ala Asp Leu Glu Asp Gly
 125 130 135

GGA TAC ACT ATC AAC ATC AAA TTT GCT GGA AAA 225
 Gly Tyr Thr Ile Asn Ile Lys Phe Ala Gly Lys
 140 145

(2) INFORMATION FOR SEQ ID NO: 18:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 75 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

(11) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 18:

Lys Glu Thr Pro Glu Thr Pro Glu Glu Pro Lys Glu Glu Val Thr Ile
 1 5 10 15

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5 Lys Val Asn Leu Ile Phe Ala Asp Gly Lys Thr Gln Thr Ala Glu Phe
 20 25 30
 Lys Gly Thr Phe Glu Glu Ala Thr Ala Glu Ala Tyr Arg Tyr Ala Asp
 35 40 45
 10 Leu Leu Ala Lys Val Asn Gly Glu Tyr Thr Ala Asp Leu Glu Asp Gly
 50 55 60
 Gly Tyr Thr Ile Asn Ile Lys Phe Ala Gly Lys
 65 70 75

15

(2) INFORMATION FOR SEQ ID NO: 19:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 249 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

20

(ii) MOLECULE TYPE: DNA (genomic)

25

(ix) FEATURE:
 (A) NAME/KEY: CDS
 (B) LOCATION: 1..246

30

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 19:

35 ATG AAC ATT AAA TTT GCT GGA AAA GAA ACA CCA GAA ACA CCA GAA GAA 48
 Met Asn Ile Lys Phe Ala Gly Lys Glu Thr Pro Glu Thr Pro Glu Glu
 1 5 10 15
 CCA AAA GAA GAA GTT ACA ATC AAA GTT AAC TTA ATC TTT GCA GAT GGA 96
 Pro Lys Glu Glu Val Thr Ile Lys Val Asn Leu Ile Phe Ala Asp Gly
 40 20 25 30
 AAG ATA CAA ACA GCA GAA CAT AAA GGA ACA TTT GAA GAA GCA ACA GCA 144
 Lys Ile Gln Thr Ala Glu His Lys Gly Thr Phe Glu Glu Ala Thr Ala
 35 40 45
 45 GAA GCT TAC AGA TAT GCA GAC TTA TTA GCA AAA GTA AAT GGC GAA TAT 192
 Glu Ala Tyr Arg Tyr Ala Asp Leu Leu Ala Lys Val Asn Gly Glu Tyr
 50 55 60
 50 ACA GCA GAC TTA GAA GAT GGT GGA AAC CAT ATG AAC ATT AAA TTT GCT 240
 Thr Ala Asp Leu Glu Asp Gly Gly Asn His Met Asn Ile Lys Phe Ala
 65 70 75 80

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GGA AAA TAA
Gly Lys

249

5

(2) INFORMATION FOR SEQ ID NO: 20:

(1) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 249 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

10

(11) MOLECULE TYPE: DNA (genomic)

15

(1x) FEATURE:

(A) NAME/KEY: CDS

(B) LOCATION: 1..246

20

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 20:

ATG AAC ATT AAA TTT GCT GGA AAA GAA ACA CCA GAA ACA CCA GAA GAA
Met Asn Ile Lys Phe Ala Gly Lys Glu Thr Pro Glu Thr Pro Glu Glu
1 5 10 15

25

48

CCA AAA GAA GAA GTT ACA ATC AAA GTT AAC TTA ATC TTT GCA GAT GGA
Pro Lys Glu Glu Val Thr Ile Lys Val Asn Leu Ile Phe Ala Asp Gly
20 25 30

30

96

AAG ATA CAA ACA GCA GAA TTC AAA GGA ACA TTT GAA GAA GCA ACA GCA
Lys Ile Gln Thr Ala Glu Phe Lys Gly Thr Phe Glu Glu Ala Thr Ala
35 40 45

35

144

GAA GCT TAC AGA AAC GCA GAC TTA TTA GCA AAA GTA AAT GGC GAA TAT
Glu Ala Tyr Arg Phe Ala Asp Leu Leu Ala Lys Val Asn Gly Glu Tyr
50 55 60

40

192

ACA GCA GAC TTA GAA GAT GGT GGA AAC CAT ATG AAC ATT AAA TTT GCT
Thr Ala Asp Leu Glu Asp Gly Gly Asn His Met Asn Ile Lys Phe Ala
65 70 75 80

240

GGA AAA TAA
Gly Lys

45

249

(2) INFORMATION FOR SEQ ID NO: 21:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 249 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

50

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(D) TOPOLOGY: linear

5 (ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

10 (A) NAME/KEY: CDS
(B) LOCATION:1..246

(x1) SEQUENCE DESCRIPTION: SEQ ID NO: 21:

15	ATG AAC ATT AAA TTT GCT GGA AAA GAA ACA CCA GAA ACA CCA GAA GAA	48
	Met Asn Ile Lys Phe Ala Gly Lys Glu Thr Pro Glu Thr Pro Glu Glu	
	1 5 10 15	
20	CCA AAA GAA GAA GTT ACA ATC AAA GTT AAC TTA ATC TTT GCA GAT GGA	96
	Pro Lys Glu Glu Val Thr Ile Lys Val Asn Leu Ile Phe Ala Asp Gly	
	20 25 30	
25	AAG ATA CAA ACA GCA GAA TTC AAA GGA ACA TTT GAA GAA GCA ACA GCA	144
	Lys Ile Gln Thr Ala Glu Phe Lys Gly Thr Phe Glu Glu Ala Thr Ala	
	35 40 45	
30	GAA GCT TAC AGA TAT GCA GAC TTA GAC GCA AAA GTA AAT GGC GAA TGG	192
	Glu Ala Tyr Arg Tyr Ala Asp Leu Asp Ala Lys Val Asn Gly Glu Trp	
	50 55 60	
35	ACA GCA GAC TTA GAA GAT GGT GGA AAC CAT ATG AAC ATT AAA TTT GCT	240
	Thr Ala Asp Leu Glu Asp Gly Gly Asn His Met Asn Ile Lys Phe Ala	
	65 70 75 80	
40	GGA AAA TAA	249
	Gly Lys	

(2) INFORMATION FOR SEQ ID NO: 22:

40 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 249 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

45 (ii) MOLECULE TYPE: DNA (genomic)

50 (ix) FEATURE:
(A) NAME/KEY: CDS
(B) LOCATION:1..246

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 22:

5	ATG AAC ATT AAA TTT GCT GGA AAA GAA ACA CCA GAA ACA CCA GAA GAA	48
	Met Asn Ile Lys Phe Ala Gly Lys Glu Thr Pro Glu Thr Pro Glu Glu	
	1 5 10 15	
10	CCA AAA GAA GAA GTT ACA ATC AAA GTT AAC TTA ATC TTT GCA GAT GGA	96
	Pro Lys Glu Glu Val Thr Ile Lys Val Asn Leu Ile Phe Ala Asp Gly	
	20 25 30	
15	AAG ATA CAA ACA GCA GAA TTC AAA GGA ACA TTT GAA GAA GCA ACA GCA	144
	Lys Ile Gln Thr Ala Glu Phe Lys Gly Thr Phe Glu Glu Ala Thr Ala	
	35 40 45	
20	GAA GCT TAC AGA TAT GCA GAC TTA CAT GCA AAA GTA AAT GGC GAA TAT	192
	Glu Ala Tyr Arg Tyr Ala Asp Leu His Ala Lys Val Asn Gly Glu Tyr	
	50 55 60	
25	ACA GCA GAC TTA GAA GAT GGT GGA AAC CAT ATG AAC ATT AAA TTT GCT	240
	Thr Ala Asp Leu Glu Asp Gly Gly Asn His Met Asn Ile Lys Phe Ala	
	65 70 75 80	
30	GGA AAA TAA	249
	Gly Lys	
35		
40		